

# SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Rad2/FEN-1 Orthologues and Uses  
Thereof

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<150> 60/112,332

<151> 1998-12-15

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Thr Arg Gln His Asn Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly
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Glu	Leu	Ala	Lys	Arg	Tyr	Ser	Lys	Arg	Asp	Asp	Ala	Thr	Lys	Asp	Leu	
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Lys	Arg	Thr	Val	Lys	Val	Thr	Arg	Gln	His	Asn	Glu	Asp	Cys	Lys	Arg	
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Ala	Ser	Glu	Asp	Met	Asp	Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu	
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Arg	His	Leu	Met	Asp	Pro	Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe	
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Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe	
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Ile	Asp	Leu	Cys	Ile	Leu	Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys	
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Gly	Ile	Gly	Gly	Gln	Thr	Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser	
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Ile	Glu	Ser	Ile	Leu	Glu	Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro	
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Glu	Asp	Trp	Pro	Tyr	Gln	Glu	Ala	Arg	Arg	Leu	Phe	Lys	Glu	Pro	Asn	
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Val	Thr	Leu	Asp	Ile	Pro	Glu	Leu	Lys	Trp	Thr	Ala	Pro	Asp	Glu	Glu	
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Val	Thr	Lys	Ala	Ile	Glu	Lys	Ile	Lys	Ser	Ala	Lys	Asn	Lys	Ser	Ser	
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Pro	Leu	Lys	Arg	Lys	Glu	Thr	Ser	Asp	Lys	Thr	Ser	Lys	Ala	Ala	Ala	
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acg	aaa	ctg	ctg	gcg	gac	aat	gcg	ccc	aag	gcg	atg	aag	gag	cag	aag	162
Thr	Lys	Leu	Leu	Ala	Asp	Asn	Ala	Pro	Lys	Ala	Met	Lys	Glu	Gln	Lys	
			10				15					20				
ttc	gag	agc	tac	ttc	ggc	cgc	aaa	atc	gcc	gtc	gac	gcc	agc	atg	agc	210

Phe	Glu	Ser	Tyr	Phe	Gly	Arg	Lys	Ile	Ala	Val	Asp	Ala	Ser	Met	Ser		
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atc	tac	cag	ttc	ctg	ata	gta	gtt	gga	agg	aca	ggc	atg	gaa	act	ctc	258	
Ile	Tyr	Gln	Phe	Leu	Ile	Val	Val	Gly	Arg	Thr	Gly	Met	Glu	Thr	Leu		
	40					45					50						
aca	aat	gaa	gct	ggg	gaa	gtc	act	agt	cat	ttg	caa	gga	atg	ttc	aac	306	
Thr	Asn	Glu	Ala	Gly	Glu	Val	Thr	Ser	His	Leu	Gln	Gly	Met	Phe	Asn		
	55				60					65					70		
cgg	aca	ata	aga	tta	ctg	gaa	gcg	gga	atc	aag	cca	gtt	tat	gtt	ttt	354	
Arg	Thr	Ile	Arg	Leu	Leu	Glu	Ala	Gly	Ile	Lys	Pro	Val	Tyr	Val	Phe		
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gat	ggc	aag	cct	cct	gat	atg	aag	aaa	caa	gaa	ctt	gct	aaa	aga	tac	402	
Asp	Gly	Lys	Pro	Pro	Asp	Met	Lys	Lys	Gln	Glu	Leu	Ala	Lys	Arg	Tyr		
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Ser	Lys	Arg	Asp	Asp	Ala	Thr	Lys	Asp	Leu	Thr	Glu	Ala	Val	Glu	Val		
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gga	gat	aaa	gat	gcg	att	gaa	aaa	ttg	agc	aag	agg	act	gta	aag	gtc	498	
Gly	Asp	Lys	Asp	Ala	Ile	Glu	Lys	Leu	Ser	Lys	Arg	Thr	Val	Lys	Val		
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aca	agg	caa	cac	aac	gaa	gat	tgt	aaa	cga	cta	tta	aga	ctt	atg	ggg	546	
Thr	Arg	Gln	His	Asn	Glu	Asp	Cys	Lys	Arg	Leu	Leu	Arg	Leu	Met	Gly		
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gtt	cct	gtt	gta	gag	gca	cct	tct	gaa	gca	gaa	gca	gaa	tgt	gca	gcc	594	
Val	Pro	Val	Val	Glu	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Glu	Cys	Ala	Ala		
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ctt	tgc	ata	aac	gat	aag	gtg	ttc	gct	gtt	gct	tca	gaa	gat	aag	gac	642	
Leu	Cys	Ile	Asn	Asp	Lys	Val	Phe	Ala	Val	Ala	Ser	Glu	Asp	Lys	Asp		
			170					175					180				
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Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu	Arg	His	Leu	Met	Asp	Pro		
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agt	tcc	aag	aaa	ata	cct	gtg	atg	gaa	ttt	gat	gtt	gcc	aag	gtt	ttg	738	
Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe	Asp	Val	Ala	Lys	Val	Leu		
	200					205					210						
gag	gag	ctt	gaa	ctc	acc	atg	gac	cag	ttc	att	gat	ttg	tgc	atc	ctg	786	
Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe	Ile	Asp	Leu	Cys	Ile	Leu		
	215				220					225					230		
tgt	gga	tgt	gac	tat	tgt	gat	agc	atc	aaa	ggg	atc	ggg	ggg	caa	aca	834	
Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys	Gly	Ile	Gly	Gly	Gln	Thr		
			235						240					245			
gct	ctg	aaa	ctt	att	cgt	caa	cat	ggg	tcc	ata	gaa	agc	atc	ttg	gag	882	
Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser	Ile	Glu	Ser	Ile	Leu	Glu		
			250					255					260				
aat	ctt	aat	aaa	gac	aga	tat	caa	att	cct	gag	gac	tgg	cct	tac	caa	930	
Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro	Glu	Asp	Trp	Pro	Tyr	Gln		
		265					270					275					

gaa gct cga cgc ttg ttc aag gag cct aat gtc act ttg gat att cct 978  
 Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro  
 280 285 290

gag cta aaa tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg 1026  
 Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu  
 295 300 305 310

gta aaa gat aat ggt ttc aat gaa gat cgg gtg aca aag gcc ata gag 1074  
 Val Lys Asp Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu  
 315 320 325

aag atc aaa tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc 1122  
 Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser  
 330 335 340

ttt ttc aag cca act gcc acc aca tca gca ccg cta aaa cgg aag gag 1170  
 Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu  
 345 350 355

act tcg gat aaa aca agc aag gca gct gcg aac aag aaa aca aag gct 1218  
 Thr Ser Asp Lys Thr Ser Lys Ala Ala Asn Lys Lys Thr Lys Ala  
 360 365 370

ggg gga aag aag aaa taatcttgga tgcttgatgt acaactacga ctacgaaagc 1273  
 Gly Gly Lys Lys Lys  
 375

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 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg  
 35 40 45  
 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His  
 50 55 60  
 Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile  
 65 70 75 80  
 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln  
 85 90 95  
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu  
 100 105 110  
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser  
 115 120 125  
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg  
 130 135 140  
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala  
 145 150 155 160

Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val  
 165 170 175  
 Ala Ser Glu Asp Lys Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu  
 180 185 190  
 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe  
 195 200 205  
 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Leu Thr Met Asp Gln Phe  
 210 215 220  
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys  
 225 230 235 240  
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser  
 245 250 255  
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro  
 260 265 270  
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn  
 275 280 285  
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu  
 290 295 300  
 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg  
 305 310 315 320  
 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser  
 325 330 335  
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala  
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 <213> Artificial Sequence

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 remove clones which have a poly(A) tail but no  
 cDNA insert.

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 36

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 <212> PRT  
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 Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln  
 35 40 45  
 Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu  
 50 55 60  
 Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys  
 65 70 75 80

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Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln
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Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gln	Glu	Val	Glu	Lys	Phe	Thr	Lys
		115					120					125			
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu
	130					135					140				
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu
145					150					155					160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala
			165						170					175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg
			180					185					190		
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His
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225					230					235					240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile
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Glu	Glu	Ile	Val	Arg	Arg	Leu	Asp	Pro	Asn	Lys	Tyr	Pro	Val	Pro	Glu
			260					265					270		
Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val
	275						280					285			
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu
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Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg
305					310					315					320
Ile	Arg	Ser	Gly	Val	Lys	Arg	Leu	Ser	Lys	Ser	Arg	Gln	Gly	Ser	Thr
			325						330					335	
Gln	Gly	Arg	Leu	Asp	Asp	Phe	Phe	Lys	Val	Thr	Gly	Ser	Leu	Ser	Ser
			340					345					350		
Ala	Lys	Arg	Lys	Glu	Pro	Glu	Pro	Lys	Gly	Ser	Thr	Lys	Lys	Lys	Ala
		355					360					365			
Lys	Thr	Gly	Ala	Ala	Gly	Lys	Phe	Lys	Arg	Gly	Lys				
	370					375					380				